

09/856275

PATENT  
ATTORNEY DOCKET NO. 44636-5046-US

532 Rec'd PCT/PTO 18 MAY 2001

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Application of: )  
 )  
 Michel RENARD et al. )  
 )  
 Application No.: ) Group Art Unit: Unassigned  
 (based on PCT/FR99/02827) )  
 )  
 Filing Date: May 18, 2001 ) Examiner: Unassigned  
 )  
 For: GENE CODING FOR AN )  
 ACYLTRANSFERASE OF OIL SEED )  
 RAPE, AND USES THEREOF )

Commissioner for Patents  
Washington, D.C. 20231  
**BOX SEQUENCE**

**STATEMENT ACCOMPANYING SEQUENCE LISTING**

Dear Sir:

The undersigned hereby states upon information and belief that the Sequence Listing submitted concurrently herewith does not include matter which goes beyond the content of the application as filed and that the information recorded on the diskette submitted concurrently herewith is identical to the written Sequence Listing submitted herewith.

Respectfully submitted,  
**MORGAN, LEWIS & BOCKIUS LLP**

Dated: 5/18/01

By: Rosanne Kosson  
Rosanne Kosson  
Registration No. 46,840

**Customer No. 009629**  
**MORGAN, LEWIS & BOCKIUS LLP**  
1800 M Street, NW  
Washington, D.C. 20036  
Tel: 202-467-7000  
Fax: 202-467-7258

SEQUENCE LISTING

<110> Renard, Michel  
Roscoe, Thomas James  
Delseny, Michel  
Bourgis, Fabienne  
Barret, Pierre  
Guerche, Philippe  
Institut National de la Recherche Agronomique  
Centre National de la Recherche Scientifique  
Universite Pierre et Marie Curie  
Universite Victor Segalen Bordeaux II

<120> Gene Coding for an Acyltransferase of Oil Seed Rape,  
and Uses Thereof

<130> 45636-5046-US

<140>  
<141>

<150> FR 98/14470  
<151> 1998-11-18

<150> PCT/FR99/02827  
<151> 1999-11-18

<160> 3

<170> PatentIn Ver. 2.1

<210> 1  
<211> 1253  
<212> DNA  
<213> Brassica napus

<220>  
<221> CDS  
<222> (58) .. (1134)  
<223> Lysophosphatidic acyltransferase (LPAAT) gene

<220>  
<221> variation  
<222> (1253)  
<223> d = a or g or t.

<400> 1  
taaaaacagc agagaaaaga gtcaagagat aaaagcaatg aagatggaga gataagc 57

atg agc aaa tct cac gga cga tgt ttt agc tcg cga gat tcc gcc atg 105  
Met Ser Lys Ser His Gly Arg Cys Phe Ser Ser Arg Asp Ser Ala Met  
1 5 10 15

gat gtc gct tct gct cgg ggg gtc tcc tca cat cct cca tat tat agc 153  
Asp Val Ala Ser Ala Arg Gly Val Ser Ser His Pro Pro Tyr Tyr Ser  
20 25 30

aaa ccc att tgt tca tca cag tca tgc ttg att cgg att ccg atc agt	201
Lys Pro Ile Cys Ser Ser Gln Ser Ser Leu Ile Arg Ile Pro Ile Ser	
35 40 45	
aaa gga tgt tgc ttt gct cgt tct tgc aac ttg att act tcc ctt cat	249
Lys Gly Cys Cys Phe Ala Arg Ser Ser Asn Leu Ile Thr Ser Leu His	
50 55 60	
gct gct tgc aga ggg gtg aca agg cgt act agt ggt gta caa tgg tgt	297
Ala Ala Ser Arg Gly Val Thr Arg Arg Thr Ser Gly Val Gln Trp Cys	
65 70 75 80	
tac cgt tct att aga ttt gac cct ttc aaa gtt aat gat aag aac tca	345
Tyr Arg Ser Ile Arg Phe Asp Pro Phe Lys Val Asn Asp Lys Asn Ser	
85 90 95	
aga act gtg act gtg aga tgc gat ctt tca gga gct gca acc cct gaa	393
Arg Thr Val Thr Val Arg Ser Asp Leu Ser Gly Ala Ala Thr Pro Glu	
100 105 110	
tct act tat cca gaa cca gag att aag ttg agc tca aga ctc aga ggg	441
Ser Thr Tyr Pro Glu Pro Glu Ile Lys Leu Ser Ser Arg Leu Arg Gly	
115 120 125	
ata tgc ttc tgt ctc gtt gct ggc atc tcc gcc att gtt ctc atc gtc	489
Ile Cys Phe Cys Leu Val Ala Gly Ile Ser Ala Ile Val Leu Ile Val	
130 135 140	
ctg atg atc att ggc cat ccc ttc gtc ctt cta ttt gat cgt tac agg	537
Leu Met Ile Ile Gly His Pro Phe Val Leu Leu Phe Asp Arg Tyr Arg	
145 150 155 160	
aga aag ttc cat cac ttc att gct aag ctt tgg gct tcc ata agc atc	585
Arg Lys Phe His His Phe Ile Ala Lys Leu Trp Ala Ser Ile Ser Ile	
165 170 175	
tac ccg ttt tac aaa aca gac atc caa ggt ttg gag aat ctg ccg tgc	633
Tyr Pro Phe Tyr Lys Thr Asp Ile Gln Gly Leu Glu Asn Leu Pro Ser	
180 185 190	
tca gac act cct tgt gta tac gtt tgc aac cac caa agc ttt ctg gat	681
Ser Asp Thr Pro Cys Val Tyr Val Ser Asn His Gln Ser Phe Leu Asp	
195 200 205	
ata tac aca ctt ctc agc ctt ggc caa agc tat aag ttc atc agc aag	729
Ile Tyr Thr Leu Leu Ser Leu Gly Gln Ser Tyr Lys Phe Ile Ser Lys	
210 215 220	
aca ggg ata ttc gtt att cct gtc atc ggt tgg gct atg tcc atg atg	777
Thr Gly Ile Phe Val Ile Pro Val Ile Gly Trp Ala Met Ser Met Met	
225 230 235 240	
ggg gtt gtt ccc ttg aag agg atg gac cca aga agc caa gtg gat tgc	825
Gly Val Val Pro Leu Lys Arg Met Asp Pro Arg Ser Gln Val Asp Cys	
245 250 255	

tta aaa cgc tgc atg gaa cta gtg aag aag gga gct tcc gtc ttt ttc	873
Leu Lys Arg Cys Met Glu Leu Val Lys Lys Gly Ala Ser Val Phe Phe	
260 265 270	
ttc cca gag gga acg agg agt aag gat ggt cgg tta ggt cct ttc aag	921
Phe Pro Glu Gly Thr Arg Ser Lys Asp Gly Arg Leu Gly Pro Phe Lys	
275 280 285	
aaa ggg gct ttt acg ata gca gct aag aca gga gtt cca gtg gtg cca	969
Lys Gly Ala Phe Thr Ile Ala Ala Lys Thr Gly Val Pro Val Val Pro	
290 295 300	
ata acg ctg atg gga aca ggg aag atc atg ccg acg ggt agt gaa ggt	1017
Ile Thr Leu Met Gly Thr Gly Lys Ile Met Pro Thr Gly Ser Glu Gly	
305 310 315 320	
ata ctg aat cat ggg gat gtg aga gtg atc atc cac aag ccg ata tat	1065
Ile Leu Asn His Gly Asp Val Arg Val Ile Ile His Lys Pro Ile Tyr	
325 330 335	
gga agc aaa gct gat gtt ctt tgc gaa gag gcg aga aac aag ata gct	1113
Gly Ser Lys Ala Asp Val Leu Cys Glu Glu Ala Arg Asn Lys Ile Ala	
340 345 350	
gaa tct atg aat ctc ttg agt tgaaacgttt gttttttaag cagtgtctct	1164
Glu Ser Met Asn Leu Leu Ser	
355	
atgaacaatg agaaggctaa accatttttta catgtcagtt ttattgttta aaataaaaatt	1224
taggcttttc aaaaaaaaaa aaaaaaaad	1253
<210> 2	
<211> 359	
<212> PRT	
<213> Brassica napus	
<400> 2	
Met Ser Lys Ser His Gly Arg Cys Phe Ser Ser Arg Asp Ser Ala Met	
1 5 10 15	
Asp Val Ala Ser Ala Arg Gly Val Ser Ser His Pro Pro Tyr Tyr Ser	
20 25 30	
Lys Pro Ile Cys Ser Ser Gln Ser Ser Leu Ile Arg Ile Pro Ile Ser	
35 40 45	
Lys Gly Cys Cys Phe Ala Arg Ser Ser Asn Leu Ile Thr Ser Leu His	
50 55 60	
Ala Ala Ser Arg Gly Val Thr Arg Arg Thr Ser Gly Val Gln Trp Cys	
65 70 75 80	
Tyr Arg Ser Ile Arg Phe Asp Pro Phe Lys Val Asn Asp Lys Asn Ser	
85 90 95	

Arg Thr Val Thr Val Arg Ser Asp Leu Ser Gly Ala Ala Thr Pro Glu  
 100 105 110  
 Ser Thr Tyr Pro Glu Pro Glu Ile Lys Leu Ser Ser Arg Leu Arg Gly  
 115 120 125  
 Ile Cys Phe Cys Leu Val Ala Gly Ile Ser Ala Ile Val Leu Ile Val  
 130 135 140  
 Leu Met Ile Ile Gly His Pro Phe Val Leu Leu Phe Asp Arg Tyr Arg  
 145 150 155 160  
 Arg Lys Phe His His Phe Ile Ala Lys Leu Trp Ala Ser Ile Ser Ile  
 165 170 175  
 Tyr Pro Phe Tyr Lys Thr Asp Ile Gln Gly Leu Glu Asn Leu Pro Ser  
 180 185 190  
 Ser Asp Thr Pro Cys Val Tyr Val Ser Asn His Gln Ser Phe Leu Asp  
 195 200 205  
 Ile Tyr Thr Leu Leu Ser Leu Gly Gln Ser Tyr Lys Phe Ile Ser Lys  
 210 215 220  
 Thr Gly Ile Phe Val Ile Pro Val Ile Gly Trp Ala Met Ser Met Met  
 225 230 235 240  
 Gly Val Val Pro Leu Lys Arg Met Asp Pro Arg Ser Gln Val Asp Cys  
 245 250 255  
 Leu Lys Arg Cys Met Glu Leu Val Lys Lys Gly Ala Ser Val Phe Phe  
 260 265 270  
 Phe Pro Glu Gly Thr Arg Ser Lys Asp Gly Arg Leu Gly Pro Phe Lys  
 275 280 285  
 Lys Gly Ala Phe Thr Ile Ala Ala Lys Thr Gly Val Pro Val Val Pro  
 290 295 300  
 Ile Thr Leu Met Gly Thr Gly Lys Ile Met Pro Thr Gly Ser Glu Gly  
 305 310 315 320  
 Ile Leu Asn His Gly Asp Val Arg Val Ile Ile His Lys Pro Ile Tyr  
 325 330 335  
 Gly Ser Lys Ala Asp Val Leu Cys Glu Glu Ala Arg Asn Lys Ile Ala  
 340 345 350  
 Glu Ser Met Asn Leu Leu Ser  
 355

<210> 3  
 <211> 7  
 <212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Consensus  
sequence of LPAATs

<220>

<221> VARIANT

<222> (3)..(6)

<223> Xaa can be any amino acid.

<400> 3

Asn His Xaa Xaa Xaa Xaa Asp

1

5

## SEQUENCE LISTING

<110> INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE  
CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE  
UNIVERSITE PIERRE ET MARIE CURIE  
UNIVERSITE VICTOR SEGALEN BORDEAUX II  
RENARD, Michel  
ROSCOE, Thomas James  
DELSENY, Michel  
BOURGIS, Fabienne  
BARRET, Pierre  
GUERCHE, Philippe

<120> GENE CODING FOR AN ACYLTRANSFERASE OF OIL SEED RAPE,  
AND USES THEREOF

<130> MJPCb539/79

<140>

<141>

<150> FR9814470

<151> 1998-11-18

<160> 2

<170> PatentIn Ver. 2.1

<210> 1

<211> 1253

<212> DNA

<213> Brassica napus

<220>

<221> CDS

<222> (58)..(1134)

<400> 1

taaaaacagc agagaaaaga gtcaagagat aaaagcaatg aagatggaga gataagc	57
atg agc aaa tct cac gga cga tgt ttt agc tcg cga gat tcc gcc atg	105
Met Ser Lys Ser His Gly Arg Cys Phe Ser Ser Arg Asp Ser Ala Met	
1 5 10 15	
gat gtc gct tct gct cgg ggg gtc tcc tca cat cct cca tat tat agc	153
Asp Val Ala Ser Ala Arg Gly Val Ser Ser His Pro Pro Tyr Tyr Ser	
20 25 30	
aaa ccc att tgt tca tca cag tca tcg ttg att cgg att ccg atc agt	201
Lys Pro Ile Cys Ser Ser Gln Ser Ser Leu Ile Arg Ile Pro Ile Ser	
35 40 45	
aaa gga tgt tgc ttt gct cgt tct tcg aac ttg att act tcc ctt cat	249
Lys Gly Cys Cys Phe Ala Arg Ser Ser Asn Leu Ile Thr Ser Leu His	
50 55 60	
gct gct tcg aga ggg gtg aca agg cgt act agt ggt gta caa tgg tgt	297
Ala Ala Ser Arg Gly Val Thr Arg Arg Thr Ser Gly Val Gln Trp Cys	
65 70 75 80	

09856275.1009001

tac cgt tct att aga ttt gac cct ttc aaa gtt aat gat aag aac tca	345
Tyr Arg Ser Ile Arg Phe Asp Pro Phe Lys Val Asn Asp Lys Asn Ser	
85 90 95	
aga act gtg act gtg aga tcg gat ctt tca gga gct gca acc cct gaa	393
Arg Thr Val Thr Val Arg Ser Asp Leu Ser Gly Ala Ala Thr Pro Glu	
100 105 110	
tct act tat cca gaa cca gag att aag ttg agc tca aga ctc aga ggg	441
Ser Thr Tyr Pro Glu Pro Glu Ile Lys Leu Ser Ser Arg Leu Arg Gly	
115 120 125	
ata tgc ttc tgt ctc gtt gct ggc atc tcc gcc att gtt ctc atc gtc	489
Ile Cys Phe Cys Leu Val Ala Gly Ile Ser Ala Ile Val Leu Ile Val	
130 135 140	
ctg atg atc att ggc cat ccc ttc gtc ctt cta ttt gat cgt tac agg	537
Leu Met Ile Ile Gly His Pro Phe Val Leu Leu Phe Asp Arg Tyr Arg	
145 150 155 160	
aga aag ttc cat cac ttc att gct aag ctt tgg gct tcc ata agc atc	585
Arg Lys Phe His His Phe Ile Ala Lys Leu Trp Ala Ser Ile Ser Ile	
165 170 175	
tac ccg ttt tac aaa aca gac atc caa ggt ttg gag aat ctg ccg tcg	633
Tyr Pro Phe Tyr Lys Thr Asp Ile Gln Gly Leu Glu Asn Leu Pro Ser	
180 185 190	
tca gac act cct tgt gta tac gtt tcg aac cac caa agc ttt ctg gat	681
Ser Asp Thr Pro Cys Val Tyr Val Ser Asn His Gln Ser Phe Leu Asp	
195 200 205	
ata tac aca ctt ctc agc ctt ggc caa agc tat aag ttc atc agc aag	729
Ile Tyr Thr Leu Leu Ser Leu Gly Gln Ser Tyr Lys Phe Ile Ser Lys	
210 215 220	
aca ggg ata ttc gtt att cct gtc atc ggt tgg gct atg tcc atg atg	777
Thr Gly Ile Phe Val Ile Pro Val Ile Gly Trp Ala Met Ser Met Met	
225 230 235 240	
ggg gtt gtt ccc ttg aag agg atg gac cca aga agc caa gtg gat tgc	825
Gly Val Val Pro Leu Lys Arg Met Asp Pro Arg Ser Gln Val Asp Cys	
245 250 255	
tta aaa cgc tgc atg gaa cta gtg aag aag gga gct tcc gtc ttt ttc	873
Leu Lys Arg Cys Met Glu Leu Val Lys Lys Gly Ala Ser Val Phe Phe	
260 265 270	
ttc cca gag gga acg agg agt aag gat ggt cgg tta ggt cct ttc aag	921
Phe Pro Glu Gly Thr Arg Ser Lys Asp Gly Arg Leu Gly Pro Phe Lys	
275 280 285	
aaa ggg gct ttt acg ata gca gct aag aca gga gtt cca gtg gtg cca	969
Lys Gly Ala Phe Thr Ile Ala Ala Lys Thr Gly Val Pro Val Val Pro	
290 295 300	
ata acg ctg atg gga aca ggg aag atc atg ccg acg ggt agt gaa ggt	1017
Ile Thr Leu Met Gly Thr Gly Lys Ile Met Pro Thr Gly Ser Glu Gly	
305 310 315 320	

10500T 5235860



<400> 2																
Met	Ser	Lys	Ser	His	Gly	Arg	Cys	Phe	Ser	Ser	Arg	Asp	Ser	Ala	Met	
1				5					10					15		
Asp	Val	Ala	Ser	Ala	Arg	Gly	Val	Ser	Ser	His	Pro	Pro	Tyr	Tyr	Ser	
			20					25					30			
Lys	Pro	Ile	Cys	Ser	Ser	Gln	Ser	Ser	Leu	Ile	Arg	Ile	Pro	Ile	Ser	
		35					40					45				
Lys	Gly	Cys	Cys	Phe	Ala	Arg	Ser	Ser	Asn	Leu	Ile	Thr	Ser	Leu	His	
	50					55					60					
Ala	Ala	Ser	Arg	Gly	Val	Thr	Arg	Arg	Thr	Ser	Gly	Val	Gln	Trp	Cys	
65					70					75					80	
Tyr	Arg	Ser	Ile	Arg	Phe	Asp	Pro	Phe	Lys	Val	Asn	Asp	Lys	Asn	Ser	
				85					90					95		
Arg	Thr	Val	Thr	Val	Arg	Ser	Asp	Leu	Ser	Gly	Ala	Ala	Thr	Pro	Glu	
			100					105					110			
Ser	Thr	Tyr	Pro	Glu	Pro	Glu	Ile	Lys	Leu	Ser	Ser	Arg	Leu	Arg	Gly	
		115					120					125				
Ile	Cys	Phe	Cys	Leu	Val	Ala	Gly	Ile	Ser	Ala	Ile	Val	Leu	Ile	Val	
	130					135					140					
Leu	Met	Ile	Ile	Gly	His	Pro	Phe	Val	Leu	Leu	Phe	Asp	Arg	Tyr	Arg	
145					150				155					160		
Arg	Lys	Phe	His	His	Phe	Ile	Ala	Lys	Leu	Trp	Ala	Ser	Ile	Ser	Ile	
			165						170					175		
Tyr	Pro	Phe	Tyr	Lys	Thr	Asp	Ile	Gln	Gly	Leu	Glu	Asn	Leu	Pro	Ser	
			180					185					190			
Ser	Asp	Thr	Pro	Cys	Val	Tyr	Val	Ser	Asn	His	Gln	Ser	Phe	Leu	Asp	
		195					200					205				

Ile Tyr Thr Leu Leu Ser Leu Gly Gln Ser Tyr Lys Phe Ile Ser Lys  
 210 215 220  
 Thr Gly Ile Phe Val Ile Pro Val Ile Gly Trp Ala Met Ser Met Met  
 225 230 235 240  
 Gly Val Val Pro Leu Lys Arg Met Asp Pro Arg Ser Gln Val Asp Cys  
 245 250 255  
 Leu Lys Arg Cys Met Glu Leu Val Lys Lys Gly Ala Ser Val Phe Phe  
 260 265 270  
 Phe Pro Glu Gly Thr Arg Ser Lys Asp Gly Arg Leu Gly Pro Phe Lys  
 275 280 285  
 Lys Gly Ala Phe Thr Ile Ala Ala Lys Thr Gly Val Pro Val Val Pro  
 290 295 300  
 Ile Thr Leu Met Gly Thr Gly Lys Ile Met Pro Thr Gly Ser Glu Gly  
 305 310 315 320  
 Ile Leu Asn His Gly Asp Val Arg Val Ile Ile His Lys Pro Ile Tyr  
 325 330 335  
 Gly Ser Lys Ala Asp Val Leu Cys Glu Glu Ala Arg Asn Lys Ile Ala  
 340 345 350  
 Glu Ser Met Asn Leu Leu Ser  
 355

093625-100901  
 FOOT " 223660